BIOTECHNOLOGY
SYSTEMS
BRANCH

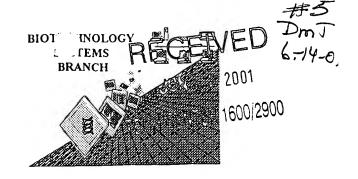RECEIVED

#5
DmJ
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2001

1600/2900

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/654, 652_

Source: _1652_

Date Processed by STIC: _5-29-01_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
     Wrapped Aminos ·   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
     prevent "wrapping."

2 ____ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ✓ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
     Numbering   use space characters, instead.

4 ____ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
     ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length   Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules,
     each n or Xaa can only represent a single residue. Please present the maximum number of each
     residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
     "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
     previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
     the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
     Artificial or Unknown sequences.

7 ____ Skipped Sequences   Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
     (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
     (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
     (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
     This sequence is intentionally skipped

     Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
     (NEW RULES)   <210> sequence id number
     <400> sequence id number
     000

9 ____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
     (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
     In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
     Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
     is Artificial Sequence

11 ____ Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
     Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
     "Unknown." Please explain source of genetic material in <220> to <223> section.
     (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
     "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
     listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

AMC – Biotechnology Systems Branch – 06/04/2001

1652

RAW SEQUENCE LISTING   DATE: 05/29/2001
PATENT APPLICATION: US/09/654,652   TIME: 15:26:36

Input Set : A:\PTO.txt
Output Set: C:\CRF3\05292001\I654652.raw

Does Not Comply
Corrected Diskette Needed
PP 1-4

```
        4 <110> APPLICANT: Shyur, Lie-Fen
        5        Chen, Jui-Lin
        6        Yang, Ning-Sun
        9 <120> TITLE OF INVENTION: A Truncated Form of Fibrobacter Succinogenes 1,3-1,4-Beta-D-
Glucanase With
       10        Improved Enzymatic Activity And Thermo-Tolerance
W--> 11 <130> FILE REFERENCE: 4910-8
W--> 12 <140> CURRENT APPLICATION NUMBER: US 09/654,652
     13 <141> CURRENT FILING DATE: 2000-09-05
W--> 14 <150> PRIOR APPLICATION NUMBER:
W--> 15 <151> PRIOR FILING DATE:
E--> 16 <160> NUMBER OF SEQ ID: 6
```

Do not include headers which have no response.

↳ Number of sequences differ:
- 6 listed
- 10 shown

ERRORED SEQUENCES

```
       18 <210> SEQ ID NO: 1
       19 <211> LENGTH: 248
       20 <212> TYPE: PRT
       21 <213> ORGANISM: Artificial Sequence
W--> 22 <220> FEATURE:
     23 <223> OTHER INFORMATION: Modified enzyme with enhanced activity and thermal stability
W--> 24 <400> SEQUENCE: 1
     25 Met Val Ser Ala Lys Asp Phe Ser Gly Ala Glu Leu Tyr Thr Leu Glu Glu Val Gln Tyr
E--> 26 1           5 .        10                 15               20
     27 Gly Lys Phe Glu Ala Arg Met Lys Met Ala Ala Ala Ser Gly Thr Val Ser Ser Met Phe
E--> 28       25       30    35                40
     29 Leu Tyr Gln Asn Gly Ser Glu Ile Ala Asp Gly Arg Pro Trp Val Glu Val Asp Ile Glu
E--> 30             45      50    55    60
     31 Val Leu Gly Lys Asn Pro Gly Ser Phe Gln Ser Asn Ile Ile Thr Gly Lys Ala Gly Ala
E--> 32       65             70              75    80
     33 Gln Lys Thr Ser Glu Lys His His Ala Val Ser Pro Ala Ala Asp Gln Ala Phe His Thr
E--> 34       85       90    95       100
     35 Tyr Gly Leu Glu Trp Thr Pro Asn Tyr Val Arg Trp Thr Val Asp Gly Gln Glu Val Arg
E--> 36     105      110   115      120
     37 Lys Thr Glu Gly Gly Gln Val Ser Asn Leu Thr Gly Thr Gln Gly Leu Arg Phe Asn Leu
E--> 38     125      130                135             140
     39 Trp Ser Ser Glu Ser Ala Ala Trp Val Gly Gln Phe Asp Glu Ser Lys Leu Pro Leu Phe
E--> 40           145      150   155      160
     41 Gln Phe Ile Asn Trp Val Lys Val Tyr Lys Tyr Thr Pro Gly Gln Gly Glu Gly Gly Ser
E--> 42     165      170   175      180
     43 Asp Phe Thr Leu Asp Trp Thr Asp Asn Phe Asp Thr Phe Asp Gly Ser Arg Trp Gly Lys
E--> 44     185      190   195      200
     45 Gly Asp Trp Thr Phe Asp Gly Asn Arg Val Asp Leu Thr Asp Lys Asn Ile Tyr Ser Arg
E--> 46             205      210               215
E--> 47 220
     48 Asp Gly Met Leu Ile Leu Ala Leu Thr Arg Lys Gly Gln Glu Ser Phe Asn Gly Gln Val
E--> 49     225      230   235      240
```

Invalid Amino Acid numbering *Use Spaces, not Tabs.* *See #3 on the Error Summary Sheet.*

file://C:\Crf3\Outhold\VsrI654652.htm   5/29/01

```
         50 Pro Arg Asp Asp Glu Pro Ala Pro
E--> 51     245
         55 <210> SEQ ID NO: 2
         56 <211> LENGTH: 267
         57 <212> TYPE: PRT
         58 <213> ORGANISM: Artificial Sequence
W--> 59 <220> FEATURE:
         60 <223> OTHER INFORMATION: Modified enzyme with enhanced activity and thermal stability
W--> 61 <400> SEQUENCE: 2
         62 Met Val Ser Ala Lys Asp Phe Ser Gly Ala Glu Leu Tyr Thr Leu Glu Glu Val Gln Tyr
E--> 63  1         5        10   15               20
         64 Gly Lys Phe Glu Ala Arg Met Lys Met Ala Ala Ala Ser Gly Thr Val Ser Ser Met Phe
E--> 65           25   30   35        40
         66 Leu Tyr Gln Asn Gly Ser Glu Ile Ala Asp Gly Arg Pro Trp Val Glu Val Asp Ile Glu
E--> 67           45        50   55        60
         68 Val Leu Gly Lys Asn Pro Gly Ser Phe Gln Ser Asn Ile Ile Thr Gly Lys Ala Gly Ala
E--> 69      65      70   75        80
         70 Gln Lys Thr Ser Glu Lys His His Ala Val Ser Pro Ala Ala Asp Gln Ala Phe His Thr
E--> 71              85        90   95        100
         72 Tyr Gly Leu Glu Trp Thr Pro Asn Tyr Val Arg Trp Thr Val Asp Gly Gln Glu Val Arg
E--> 73      105       110  115       120
         74 Lys Thr Glu Gly Gly Gln Val Ser Asn Leu Thr Gly Thr Gln Gly Leu Arg Phe Asn Leu
E--> 75      125                 130                   135                   140
         76 Trp Ser Ser Glu Ser Ala Ala Trp Val Gly Gln Phe Asp Glu Ser Lys Leu Pro Leu Phe
E--> 77           145       150  155       160
         78 Gln Phe Ile Asn Trp Val Lys Val Tyr Lys Tyr Thr Pro Gly Gln Gly Glu Gly Gly Ser
E--> 79      165       170  175       180
         80 Asp Phe Thr Leu Asp Trp Thr Asp Asn Phe Asp Thr Phe Asp Gly Ser Arg Trp Gly Lys
E--> 81           185       190  195       200
         82 Gly Asp Trp Thr Phe Asp Gly Asn Arg Val Asp Leu Thr Asp Lys Asn Ile Tyr Ser Arg
E--> 83                     205                 210             215       220
         84 Asp Gly Met Leu Ile Leu Ala Leu Thr Arg Lys Gly Gln Glu Ser Phe Asn Gly Gln Val
E--> 85      225       230  235       240
         86 Pro Arg Asp Asp Glu Pro Ala Pro Asn Ser Ser Ser Val Asp Lys Leu Ala Ala Ala Leu
E--> 87      245       250  255       260
         88 Glu His His His His His His
E--> 89      265
         91 <210> SEQ ID NO: 3
         92 <211> LENGTH: 349
         93 <212> TYPE: PRT
         94 <213> ORGANISM: Fibrobacter succinogenes
W--> 95 <220> FEATURE:
         96 <223> OTHER INFORMATION:
W--> 97 <400> SEQUENCE: 3
         98 Met Asn Ile Lys Lys Thr Ala Val Lys Ser Ala Leu Ala Val Ala Ala Ala Ala Ala Ala
E--> 99  1         5        10   15        20
        100 Leu Thr Thr Asn Val Ser Ala Lys Asp Phe Ser Gly Ala Glu Leu Tyr Thr Leu Glu Glu
E--> 101     25   30   35        40
        102 Val Gln Tyr Gly Lys Phe Glu Ala Arg Met Lys Met Ala Ala Ala Ser Gly Thr Val Ser
```

(handwritten annotations in right margin:) Invalid Amino Acid numbers See p.1

(handwritten annotation at bottom:) Invalid amino acid numbering. See p.1

```
E--> 103      45      50      55      60
     104 Ser Met Phe Leu Tyr Gln Asn Gly Ser Glu Ile Ala Asp Gly Arg Pro Trp Val Glu Val
E--> 105              65              70   75      80
     106 Asp Ile Glu Val Leu Gly Lys Asn Pro Gly Ser Phe Gln Ser Asn Ile Ile Thr Gly Lys
E--> 107      85      90   95     100
     108 Ala Gly Ala Gln Lys Thr Ser Glu Lys His His Ala Val Ser Pro Ala Ala Asp Gln Ala
E--> 109          105     110 115     120
     110 Phe His Thr Tyr Gly Leu Glu Trp Thr Pro Asn Tyr Val Arg Trp Thr Val Asp Gly Gln
E--> 111    125     130 135     140
     112 Glu Val Arg Lys Thr Glu Gly Gly Gln Val Ser Asn Leu Thr Gly Thr Gln Gly Leu Arg
E--> 113              145          150              155              160
     114 Phe Asn Leu Trp Ser Ser Glu Ser Ala Ala Trp Val Gly Gln Phe Asp Glu Ser Lys Leu
E--> 115          165     170          175     180
     116 Pro Leu Phe Gln Phe Ile Asn Trp Val Lys Val Tyr Lys Tyr Thr Pro Gly Gln Gly Glu
E--> 117      185     190 195     200
     118 Gly Gly Ser Asp Phe Thr Leu Asp Trp Thr Asp Asn Phe Asp Thr Phe Asp Gly Ser Arg
E--> 119   205     210 215     220
     120 Trp Gly Lys Gly Asp Trp Thr Phe Asp Gly Asn Arg Val Asp Leu Thr Asp Lys Asn Ile
E--> 121   225     230 235     240
     122 Tyr Ser Arg Asp Gly Met Leu Ile Leu Ala Leu Thr Arg Lys Gly Gln Glu Ser Phe Asn
E--> 123   245     250 255     260
     124 Gly Gln Val Pro Arg Asp Asp Glu Pro Ala Pro Gln Ser Ser Ser Ser Ala Pro Ala Ser
E--> 125   265     270 275     280
     126 Ser Ser Ser Val Pro Ala Ser Ser Ser Ser Val Pro Ala Ser Ser Ser Ser Ala Phe Val
E--> 127   285     290 295     300
     128 Pro Pro Ser Ser Ser Ser Ala Thr Asn Ala Ile His Gly Met Arg Thr Thr Pro Ala Val
E--> 129   305     310 315     320
     130 Ala Lys Glu His Arg Asn Leu Val Asn Ala Lys Gly Ala Lys Val Asn Pro Asn Gly His
E--> 131   325     330 335     340
     132 Lys Arg Tyr Arg Val Asn Phe Glu His
E--> 133   345
     210 <210> SEQ ID NO: 7
     211 <211> LENGTH: (13)
     212 <212> TYPE: DNA
     213 <213> ORGANISM: Artificial Sequence
W--> 214 <220> FEATURE:
     215 <223> OTHER INFORMATION: PCR primer
W--> 216 <400> SEQUENCE: 7
E--> 217 tcaccaccat ggttagcgca aag        (13)
     219 <210> SEQ ID NO: 8
     220 <211> LENGTH: (15)
     221 <212> TYPE: DNA
     222 <213> ORGANISM: Artificial Sequence
W--> 223 <220> FEATURE:
     224 <223> OTHER INFORMATION: PCR primer
W--> 225 <400> SEQUENCE: 8
E--> 226 gccacgaatt ctgttcaaag ttcac      (15)
     228 <210> SEQ ID NO: 9
     229 <211> LENGTH: (17)
```

Handwritten annotations:

Invalid amino acid numbering. See p.1

Seq #7
- 13 listed
- 23 shown

Seq #8
- 15 listed
- 25 shown

RAW SEQUENCE LISTING　　　　　　　　DATE: 05/29/2001
PATENT APPLICATION:　**US/09/654,652**　　TIME: 15:26:36

　　　　Input Set : **A:\PTO.txt**
　　　　Output Set: **C:\CRF3\05292001\I654652.raw**

```
        230 <212> TYPE: DNA
        231 <213> ORGANISM: Artificial Sequence
W-->    232 <220> FEATURE:
        233 <223> OTHER INFORMATION: PCR Primer
W-->    234 <400> SEQUENCE: 9
E-->    235 cagccggcga tggccatggt tagcgca      (17)
        237 <210> SEQ ID NO: 10
        238 <211> LENGTH: (19)
        239 <212> TYPE: DNA
        240 <213> ORGANISM: Artificial Sequence
W-->    241 <220> FEATURE:
        242 <223> OTHER INFORMATION: PCR Primer
W-->    243 <400> SEQUENCE: 10
E-->    244 ctgctagaag aattcggagc aggttcgtc    (19)
```
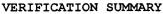
Seq #9
- 17 listed
- 27 shown

Seq # 10
- 19 listed
- 29 shown

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/654,652**

DATE: 05/29/2001
TIME: 15:26:37

Input Set : **A:\PTO.txt**
Output Set: **C:\CRF3\05292001\I654652.raw**

```
L:11 M:283 W: Missing Blank Line separator, <130> field identifier
L:12 M:283 W: Missing Blank Line separator, <140> field identifier
L:14 M:256 W: Invalid Numeric Header Field, <150> PRIOR APPLICATION NUMBER:
L:15 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:16 M:283 W: Missing Blank Line separator, <160> field identifier
L:22 M:283 W: Missing Blank Line separator, <220> field identifier
L:24 M:283 W: Missing Blank Line separator, <400> field identifier
L:26 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:28 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:30 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:32 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:34 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:36 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:38 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:40 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:42 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:44 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:46 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:47 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:49 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:51 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:59 M:283 W: Missing Blank Line separator, <220> field identifier
L:61 M:283 W: Missing Blank Line separator, <400> field identifier
L:63 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:65 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:67 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:69 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:71 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:73 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:75 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:77 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:79 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:81 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:83 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:85 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:87 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:89 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:95 M:283 W: Missing Blank Line separator, <220> field identifier
L:97 M:283 W: Missing Blank Line separator, <400> field identifier
L:99 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:101 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:103 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:105 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:107 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:109 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:111 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:113 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:115 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
```

```
L:117 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:119 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:121 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:123 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:125 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:127 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:129 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:131 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:133 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:139 M:283 W: Missing Blank Line separator, <220> field identifier
L:141 M:283 W: Missing Blank Line separator, <400> field identifier
L:162 M:283 W: Missing Blank Line separator, <220> field identifier
L:164 M:283 W: Missing Blank Line separator, <400> field identifier
L:187 M:283 W: Missing Blank Line separator, <220> field identifier
L:189 M:283 W: Missing Blank Line separator, <400> field identifier
L:214 M:283 W: Missing Blank Line separator, <220> field identifier
L:216 M:283 W: Missing Blank Line separator, <400> field identifier
L:217 M:254 E: No. of Bases conflict, LENGTH:Input:13 Counted:23 SEQ:7
L:217 M:252 E: No. of Seq. differs, <211>LENGTH:Input:13 Found:23 SEQ:7
L:223 M:283 W: Missing Blank Line separator, <220> field identifier
L:225 M:283 W: Missing Blank Line separator, <400> field identifier
L:226 M:254 E: No. of Bases conflict, LENGTH:Input:15 Counted:25 SEQ:8
L:226 M:252 E: No. of Seq. differs, <211>LENGTH:Input:15 Found:25 SEQ:8
L:232 M:283 W: Missing Blank Line separator, <220> field identifier
L:234 M:283 W: Missing Blank Line separator, <400> field identifier
L:235 M:254 E: No. of Bases conflict, LENGTH:Input:17 Counted:27 SEQ:9
L:235 M:252 E: No. of Seq. differs, <211>LENGTH:Input:17 Found:27 SEQ:9
L:241 M:283 W: Missing Blank Line separator, <220> field identifier
L:243 M:283 W: Missing Blank Line separator, <400> field identifier
L:244 M:254 E: No. of Bases conflict, LENGTH:Input:19 Counted:29 SEQ:10
L:244 M:252 E: No. of Seq. differs, <211>LENGTH:Input:19 Found:29 SEQ:10
L:16 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (6) Counted (10)
```

5/29/01